

GENETIC VARIABILITY, DIVERGENCE AND CORRELATION STUDIES IN BRINJAL

RESHMIKA. P. K

Research Scholar, Department of Olericulture, College of Horticulture, Kerala Agricultural University, Kerala, India

ABSTRACT

Brinjal (Solanum melongena L.) a member of the family solanaceae has the chromosome number $2n=24$. Brinjal originated in India and is one of the most popular and major vegetable crop grown in South Asia and other parts of the world. In India brinjal is grown in an area of 7.11 lakh hectares with the production of 135.57 lakh tonnes and the productivity is 19.1 tonnes per hectare (Anon., 2013).

Planning and execution of a breeding program for the improvement of quantitative attributes depends to the greater extent upon the magnitude of genetic variability and divergence existing in the germplasm. Selection of genotype is based upon the association of characteristics. Correlation coefficients become more evident when they are partitioned into their components in path analysis (Kalloo, 1994).

The existing variability can be used to further enhance the yield level of the brinjal cultivars by following appropriate breeding strategies. Diverse genotypes can be utilized for hybridization programme also. Emphasis must be given to the characters having high direct and positive effect on yield like number of fruits per plant and fruit weight.

KEYWORDS: *Brinjal, Variability, Divergence, Correlation, Path Analysis*

Received: Oct 19, 2015; **Accepted:** Oct 28, 2015; **Published:** Nov 02, 2015; **Paper Id.:** IJASRDEC201514

INTRODUCTION

A wide survey of genetic variability and a thorough understanding of the genetic makeup of the crop with the biometrical tools is very much indispensable for an initiating an effective breeding programme. Study of genetic divergence in existing germplasm in selecting the parents for hybridization is more realistic. Association of characteristics among yield, its components, and other economical traits is important for making selection in the breeding program. It suggests the advantage of a scheme of selection for more than one character at a time. Path coefficient analysis permits the separation of the direct effects from indirect effects through other related characters by partitioning the correlation coefficients.

Genetic Variability

The phenotypic expression of the plant character is mainly controlled by the genetic make up of the plant and the environment, in which it is grown and the interaction between the genotypes and environment. Further, the genetic variance of any quantitative trait is composed of additive variance (heritable) and non additive variance (non heritable), which include dominance and epistasis (non-allelic interaction).

It is necessary to partition the observed phenotypic variability into its heritable and non heritable components with suitable parameters, such as phenotypic and genotypic coefficient of variation and heritability in

broad sense. Effectiveness of selection directly depends on the amount of heritability and genetic advance as per cent of mean for that character.

Shekar *et al.* (2012) reported the estimates of variability, heritability and genetic advance as percent of mean for fourteen characters in 31 germplasm accessions of brinjal. Highly significant differences were observed among the accessions. High phenotypic and genotypic coefficient of variation was observed for number of leaves per plant, leaf area index, number of fruits per plant, average fruit length, average fruit diameter, fruit yield per plant, fruit yield per plot, fruit yield per hectare. Almost all the characters exhibited high heritability except for plant height (51%) and moderate to low heritability was recorded for average fruit weight (24%). Highest genetic advance as percent of mean was observed for almost all the characters except for days to first flowering, days to first picking, plant height and average fruit weight recorded moderate to low genetic advance as per cent of mean. High estimates of PCV and GCV and high estimates of heritability coupled with high estimates of genetic advance for number of leaves per plant, number of branches per plant, leaf area index, number of fruits per plant, average fruit length, average fruit diameter, fruit yield per plant, yield per plot and total number of harvests indicated that the variability available for these traits in the germplasm was high and selection for these traits may be effective. Low heritability and low genetic advance were observed for the character average fruit weight. These results revealed the predominance of both additive and non-additive gene action in the above mentioned characters.

Kumar *et al.* (2013 b) studied on genetic variability for quantitative and qualitative characters in brinjal. The genetic architecture of fruit yield is based on the balance or overall net effect produced by various yield components interacting with one another. Based on the studies on genetic variability, it may be concluded that, the characters fruit length, calyx length, number of fruits per plant, little leaf incidence, total phenol content and fruit yield per plant recorded high amount of genetic variability along with heritability and genetic advance. So additive gene action is present. This reveals that there is a greater scope for improving these characters by simple phenotypic selection. Days to first flowering, which was found to be under the influence of non - additive gene action, suggested that heterosis breeding is the best to improve this trait.

Thirty two eggplant germplasm accessions used in the study by Arivalagan *et al.* (2013) were obtained from National Gene Bank, National Bureau of Plant Genetic Resources (NBPGR), New Delhi, India. Five fruits per plant were harvested at marketable maturity stage and analyzed for macro- and micro-minerals. Highest mean value was obtained for the mineral Potassium (231.831 mg/100 g). Phenotypic co-efficient of variation and genotypic co-efficient of variation were high for the minerals studied except potassium. The broad sense heritability for micro- and macro minerals was more than 84% with maximum of 97.06% for magnesium followed by potassium. The expected genetic advance as percentage of mean ranged from 19.69 to 85.96%. Maximum genetic gain was observed for copper (85.96%) followed by iron (55.39%). Potassium showed low genetic gain (19.69%). Heritability estimates along with genetic advance are more useful in predicting the resultant effect for the selection of the best individuals from a population. The heritability and genetic advance values were high for copper, zinc and followed by iron, suggests that these traits are under additive gene action and significant improvement can be obtained for these traits. Two germplasm accessions, IC090785 and IC383102 have been identified as rich sources for all minerals studied. Hence, these two accessions could be utilized further in breeding programme for developing mineral rich varieties of eggplant.

Genetic Diversity

Eggplant or brinjal was first cultivated in India which is regarded as the primary centre of origin/diversity. Information on genetic divergence among the available germplasm is vital to a plant breeder for an efficient choice of parents for hybridization. It is an established fact that genetically diverse parents are likely to contribute desirable segregants. It was also observed that the more diverse the parents, greater are the chances of obtaining high heterotic F_1 s and broad spectrum of variability in the segregating generation (Arunachalam, 1981). Improvement in yield and quality is normally achieved by selecting genotypes with desirable character combinations existing in the nature or by hybridization. Selection of parents identified on the basis of divergence analysis would be more promising for a hybridization programme. Of the several methods available, Mahalanobis generalized distance estimated by D^2 statistic (Rao, 1952) is a unique method for disseminating populations considering a set of parameters together rather than inferring from indices based upon morphological similarities, eco-geographical diversity and phylogenetic relationships.

Kumar *et al.* (2013 a) evaluated fourteen genotypes for fifteen characters and the analysis revealed the presence of wide genetic diversity as they formed six gene constellations. Among the six clusters, cluster III had constituted maximum of five genotypes out of fourteen assembled from different geographical location. The clustering pattern revealed that the genotype did not resolve according to their geographical origin. Geographic diversity, though appear as an important factors it seems that it is not the only factor determining the genetic divergence. It also indicates that the factors other than geographical diversity may also be responsible for such grouping types. The values show that the cluster V had the maximum intra D^2 value, followed by cluster III. This is indicative of the fact that the genotypes included in these clusters are very diverse. The inter cluster D^2 value was found to be maximum between cluster II and V followed by IV and V. The genotypes belonging to clusters II, II, IV and V could have greater genetic divergence and hence inter mating between the genotypes belonging to them would give more transgressive segregates in advanced generations.

Genetic diversity among a group of accesses estimated from different sets of characteristics obtained at different stages of development (Silva *et al.*, 2001). The diversity varies in relation to each considered set. Therefore, with respect to vegetative and reproductive characteristics the most divergent accesses were L4 ('Florida Market') and L10 (PI 166995), while L4 and L12 ('Indiana') were the most divergent for the productive characteristics. Vegetative stage characteristics grouped the accesses into two clusters, reproductive stage characters into four and the productive stage ones into six clusters. Divergence estimates were positively correlated, and the significance of this correlation decreases as the stages of development become more distant. However, the number and composition of clusters varies from one stage to another, suggesting that the estimated genetic divergence among accesses is related only to the variability existing in the characteristics used for their estimation, not allowing extrapolations to other non-analyzed characters.

Behera *et.al* (1999) studied about 12 genotypes of eggplant with respect to fruit-and-shoot borer resistance. The intra cluster average D^2 value ranged from 0 to 4.461. Among the clusters, cluster I (*Solanum gilo*, *Solanum anomalum* and *Solanum incanum*) had maximum intra-cluster distance (4.461) and cluster III (*Solanum indicum*) the minimum (0). The minimum inter cluster distance (2.721) was between clusters I and IV (Pusa Purple Cluster, Bhagyamathi, Annamalai, APAU-4, Nurki and Singhnath) whereas maximum between clusters II (Aushey and Pusa Kranti) and III (9.618). The least intra cluster divergence (2.673) recorded in cluster IV indicated that the genotypes Pusa Purple Cluster, Bhagyamathi, Annamalai, APAU 4, Nurki and Singhnath were quite close to each other genetically. Highest intra cluster divergence (4.461) was recorded in cluster I, which indicated limited gene exchange between these *Solanum* species. The clusters II

and III were most divergent showing highest inter cluster distance (92.506), whereas the inter cluster distance between cluster I and and IV was the lowest. This shows that hybridization of genotypes belonging to different clusters can be used for exploiting hybrid vigour and for obtaining good segregates for resistance to shoot and fruit borer.

Eleven RAPD primers were used to analyse the genetic variation in 29 popular Indian brinjal varieties (Verma *et al.*, 2012). Sixty four polymorphic markers were generated with an average of 5.81 polymorphic bands per primer. UPGMA clustering for RAPD grouped all the brinjal varieties into two clusters. The average similarity coefficient by RAPD analysis is 0.67. The main group consisted of one large sub cluster (9 genotypes, viz., NDB-25, DBL-21, SL-195, Green Long, KS-327, SL-91-2, KS-331, PPC and Pusa Kranti) and 6 small sub-clusters (2-3 genotypes). It was observed from the dendrogram that DBR-31 is genetically diverse from the rest of the 28 genotypes. High degree of variation reported in the present study could be due to the fact that our analysis included genotypes from India where greatest diversity is reported. Interestingly collections originating from various parts of the country did not form well defined distinct groups and were interspersed with each other indicating no association between RAPD pattern and geographic origin of accessions.

Correlation and Path Analysis

Variability studies provide information on the extent of improvement possible in different characters, but they do not throw light on the extent and nature of relationship existing between yield and various contributory characters. As a rational approach for the improvement of yield, selection has to be made for components of yield, since there may not be gene for yield *per se* but for various yield components. Further, many of these yield contributing characters are interacted in desirable and undesirable direction. Hence, a knowledge regarding the association of various characters among themselves and with economic characters is necessary for making indirect selection for improvement of economic characters. Character association or correlation is a measure of the degree of association between two characters.

Though correlation analysis indicates the association pattern of components traits with yield, they simply represent the overall influence of a particular trait on yield rather than providing cause and effect relationship. The technique of path coefficient analysis developed by Wright (1921) and demonstrated by Dewey and Lu (1959) facilitates the partitioning of correlation coefficients into direct and indirect contribution of various characters on yield. It is standardized partial regression coefficient analysis. As such, it measures the direct influence of one variable upon other. Such information would be of great value in enabling the breeder to specifically identify the important component traits of yield and utilize the genetic stock for improvement in a planned way. Path analysis also measures the relative importance of causal factors involved. This is simply a standardized partial regression analysis, where in total correlation values were subdivided into individual causal factors.

Arunkumar *et al.* (2013) studied on the correlation aspects. Fruit yield per plant was found to be significantly and positively correlated with number of branches per plant, fruit breadth, number of fruits per plant and average fruit weight, both at genotypic as well as phenotypic levels. The correlation for days to 50 % flowering with fruit breadth and average fruit weight was positive and significant. Plant height showed significant positive association with number of branches per plant, fruit length, fruit breadth and average fruit weight. Number of branches per plant showed significant association with average fruit weight, while fruit length showed positive correlation with fruit breadth. Fruit breadth expressed significant positive association with average fruit weight. Number of fruits per plant had positive direct effect on fruit yield per plant, followed by average fruit weight. Average fruit weight had positive and direct effect on number of fruits per plant followed

by fruit breadth and days to 50% flowering. Fruit length had negative direct effect on fruit yield per plant. Fruit breadth had positive indirect effects with fruit yield per plant, via average fruit weight, number of fruits per plant. The positive direct effect of days to 50 % flowering was manifested through indirect positive effects via, average fruit weight, fruit breadth, fruit length and number of branches per plant. Thus for developing high yielding brinjal genotypes emphasis should be placed on number of fruits per plant, average fruit weight, fruit breadth and days to 50% flowering.

Ahmed *et al.* (2009) reported that shoot infestation rate was found to be positively correlated with plant height (0.407), stem diameter (0.520), number of branches plant⁻¹ (0.255), number of leaves plant⁻¹ (0.478), third leaf length (0.373) and width (0.536). The estimated correlation coefficients among shoot infestation caused by brinjal shoot and fruit borer and tested leaf and shoot characters were partitioned into direct and indirect effects and have been presented by path coefficient analysis. The direct effect of plant height and stem diameter, number of leaves plant⁻¹ and third leaf width against shoot infestation caused by BSFB were positive (0.396, 0.248, 0.059 and 0.393 respectively) and higher in magnitude at 1% level of significance. The direct effect of number of branches plant⁻¹ and third leaf length against shoot infestation were negative (-0.082 and -0.067 respectively) and lower in magnitude at 5% level of significance. It was observed that the higher plant height, stem diameter, third leaf width and more number of leaves increased infestation of BSFB, because more leaves and higher third leaf width may be suitable for oviposition and thick stem associated with succulent, thin cuticle and soft parenchymatous cells may be suitable to bore easily by young larvae. On the other hand, higher number of branches plant⁻¹ reduced infestation because it may be reduced stem diameter.

The fruit yield per plant had significant positive correlation with total soluble sugars and reducing sugars at both genotypic and phenotypic levels, and with total phenols at genotypic level only. While, the correlation between fruit yield and dry matter was found negative and significant. The fruit borer infested fruits was positively and significantly correlated with anthocyanin content, total soluble sugars and reducing sugars at both the levels. Whereas, its association with polyphenoloxidase activity, total phenols and glycoalkaloid content was found negative and significant. Little leaf disease which is considered to be serious damaging to the crop was significantly and positively correlated with anthocyanin content. However, the association of this trait with glycoalkaloid content and total phenols was observed to be negative and significant.

Total soluble sugars and reducing sugars had negative significant association with total phenols and glycoalkaloid content. While the association between these two traits was found to be significant and positive. The results of the present investigation suggested that fruit yield per plant can be improved by selecting genotypes having higher total soluble and reducing sugars, total phenols and lower dry matter. It also suggested that selection of genotypes having higher glycoalkaloid content, total phenols and high polyphenoloxidase activity; moderate soluble and reducing sugars; and low anthocyanin content may help in improving resistance against fruit borer infestation and little leaf incidence without compromising fruit yield potential in brinjal (Doshi *et al.*, 1998).

Genotypic correlation of shoot and fruit borer infestation with total phenols polyphenoloxidase activity and glycoalkaloid content were negative and significant. However this trait had positive and significant genotypic association with total soluble sugars, anthocyanin content and reducing sugars. Total soluble sugars, reducing sugars and anthocyanin content had high positive and direct effect except anthocyanin content which have high indirect effect via total soluble sugars. Total phenols, polyphenoloxidase activity and glycoalkaloid content had a high negative direct effect on shoot and

fruit borer infestation. Genotypes having high phenols, glycoalkaloid and polyphenoloxidase activity and lower in total soluble sugar, reducing sugars and anthocyanin content could be utilized in the breeding programme for the development of shoot and fruit borer pest resistance varieties in egg plant crop (Doshi , 2004,).

CONCLUSIONS

Being primary centre of origin, India has accumulated a wide range of variability in brinjal. The existing variability can be used to further enhance the yield level of the brinjal cultivars by following appropriate breeding strategies. Diverse genotypes can be utilized for hybridization programme also. Major yield contributing characters is identified and selection for these traits will be helpful in getting increased yield of this crop. Emphasis must be given to the characters having high direct and positive effect on yield like number of fruits per plant and fruit weight.

REFERENCES

1. Ahmed, H., Rahman, M. H., Haque, M. A. & Ahmed, K. S. (2009). Studies on shoot and leaf characters of brinjal plants and their quantitative relationships with brinjal shoot and fruit borer. *Journal of Bangladesh Agricultural University*, 7, 29-32
2. Anonymous, 2013, *Indian Horticulture Database*, Retrieved from <http://www.nbhb.gov.in>
3. Arivalagan, M., Bhardwaj, R., Gangopadhyay, K. K., Prasad, T. V. & Sarkar, S. K. (2013). Mineral composition and their genetic variability analysis in egg plant (*Solanum melongena* L.) germplasm. *Journal of Applied Biotechnology and Food Quality*, 86, 99-103
4. Arunachalam, V. (1981). Genetic distances in plant breeding. *Indian Journal of Genetics*, 41, 226-236
5. Arunkumar, B., Kumar, S. V. S. & Prakash, C. G. (2013). Genetic variability and divergence studies in brinjal (*Solanum melongena* L.). *Bioinfolet*, 10, 739-744.
6. Behera, T. K., Singh, N. & Kalda, T. S. (1999). Genetic diversity in egg plant for resistance to shoot and fruit borer. *Indian Journal of Horticulture*, 56, 259-261
7. Dewey, D. H. & Lu, K. H. (1959). A correlation and path analysis of components of crested wheat grass production. *Agronomy Journal*, 51, 515-518
8. Doshi, K. M. (2004). Influence of biochemical factors of shoot and fruit borer infestation in eggplant. *Capsicum and Eggplant Newsletter*, 23, 145-148
9. Doshi, K. M., Bhalala, M. K. & Kathiria, K. B. (1998). Correlation and path analysis for yield, fruit borer infestation, little leaf incidence and quality traits in brinjal (*Solanum melongena* L.). *Capsicum and Eggplant Newsletter*, 17, 84-87
10. Kalloo, G. (1994). *Vegetable breeding*. New Delhi: Panima Educational Book Agency
11. Kumar, S. R., Arumugam, T. & Anandakumar, C. R. (2013a). Genetic diversity in egg plant (*Solanum melongena* L.). *Plant Gene and Trait*, 4, 4-8
12. Kumar, S. R., Arumugam, T., Anandakumar, C. R. & Premalakshmi, V. (2013b). Genetic variability for quantitative and qualitative characters in brinjal (*Solanum melongena* L.). *African Journal of Agricultural Research*, 8, 4956-4959
13. Rao, C. R. (1952). *Advanced statistical methods in Biometrics Research*. New York: John Wiley and Sons
14. Shekar, C. K., Ashok, P. & Sasikala, K. (2012). Studies on heritability and multivariate analyses in brinjal (*Solanum melongena* L.). *Vegetable Crops Research Bulletin*, 76, 79-88
15. Silva, D. J. H. D., Costa, C. P. D., Cruz, C. M., Casali, V. W. D. & Dias, L. A. D. S. (2001). Stability of genetic divergence

- among eggplant accesses in three stages of development. Crop Breeding and Applied Biotechnology, 1, 135-143*
16. Verma, M., Rath, S., Munshi, A. D., Kumar, A., Arya, L., Bhat, K. V. & Kumar, R. (2012) Genetic diversity of Indian brinjal revealed by RAPD and SSR markers. *Indian Journal of Horticulture*, 69, 517-522
 17. Wright, S. (1921). *Correlation and causation. Journal of Agricultural Research*, 20, 557-587

